An official website of the United States government Here's how you know

putative spike glycoprotein [Zaria bat coronavirus]

GenBank: ADY17911.1

Identical Proteins FASTA Graphics

Go to:

```
LOCUS       ADY17911                1298 aa            linear   VRL 25-JUL-2016
DEFINITION  putative spike glycoprotein [Zaria bat coronavirus].
ACCESSION   ADY17911
VERSION     ADY17911.1
DBSOURCE    accession HQ166910.1
KEYWORDS    .
SOURCE      Zaria bat coronavirus
  ORGANISM  Zaria bat coronavirus
            Viruses; Riboviria; Orthornavirae; Pisuviricota; Pisoniviricetes;
            Nidovirales; Cornidovirineae; Coronaviridae; Orthocoronavirinae;
            Betacoronavirus; Hibecovirus.
REFERENCE   1  (residues 1 to 1298)
  AUTHORS   Quan,P.L., Firth,C., Street,C., Henriquez,J.A., Petrosov,A.,
            Tashmukhamedova,A., Hutchison,S.K., Egholm,M., Osinubi,M.O.,
            Niezgoda,M., Ogunkoya,A.B., Briese,T., Rupprecht,C.E. and
            Lipkin,W.I.
  TITLE     Identification of a severe acute respiratory syndrome
            coronavirus-like virus in a leaf-nosed bat in Nigeria
  JOURNAL   MBio 1 (4), e00208-10 (2010)
   PUBMED   21063474
  REMARK    Publication Status: Online-Only
REFERENCE   2  (residues 1 to 1298)
  AUTHORS   Quan,P.-L., Firth,C., Street,C., Henriquez,J.A., Petrosov,A.,
            Tashmukhamedova,A., Briese,T. and Lipkin,W.I.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-AUG-2010) Center for Infection and Immunity, Columbia
            University, 720 West 168 th, NY, NY 10032, USA
COMMENT     Method: conceptual translation supplied by author.
FEATURES             Location/Qualifiers
     source          1..1298
                     /organism="Zaria bat coronavirus"
                     /strain="ZBCoV"
                     /isolation_source="gastrointestinal tract"
                     /host="Hipposideros commersoni"
                     /db_xref="taxon:989337"
                     /country="Nigeria"
                     /collection_date="2008"
     Protein         1..1298
                     /product="putative spike glycoprotein"
     Region          22..319
                     /region_name="SARS-CoV-like_Spike_S1_NTD"
                     /note="N-terminal domain of the S1 subunit of the Spike
                     (S) protein from Severe acute respiratory syndrome
                     coronavirus and related betacoronaviruses in the B
                     lineage; cd21624"
                     /db_xref="CDD:394950"
     Site            order(50,53..56,134,136,191,223..225,252,255,257..261,
                     296..298)
                     /site_type="other"
                     /note="trimer interface [polypeptide binding]"
                     /db_xref="CDD:394950"
     Region          335..>462
                     /region_name="CoV_Spike_S1_RBD"
                     /note="receptor-binding domain of the S1 subunit of
                     coronavirus spike (S) proteins; cl40478"
                     /db_xref="CDD:424109"
     Site            order(376,395..398,402..405,407,411,417,426..427,429,
                     435..436,438,445,448)
                     /site_type="other"
                     /note="trimer interface [polypeptide binding]"
                     /db_xref="CDD:394823"
     Region          569..1231
                     /region_name="betaCoV_Spike_SD1-2_S1-S2_S2"
                     /note="SD-1 and SD-2 subdomains, the S1/S2 cleavage
                     region, and the S2 fusion subunit of the spike (S)
                     glycoprotein from betacoronaviruses; cd22370"
                     /db_xref="CDD:411957"
     Site            order(699..701,718..723,737)
                     /site_type="other"
                     /note="S1/S2 cleavage region"
                     /db_xref="CDD:411957"
     Site            828..836
                     /site_type="other"
                     /note="fusion peptide"
                     /db_xref="CDD:411957"
     Site            850..867
                     /site_type="other"
                     /note="internal fusion peptide"
                     /db_xref="CDD:411957"
     Region          941..1006
                     /region_name="heptad repeat 1"
                     /note="heptad repeat 1 [structural motif]"
                     /db_xref="CDD:411957"
     Region          1190..1231
                     /region_name="heptad repeat 2"
                     /note="heptad repeat 2 [structural motif]"
                     /db_xref="CDD:411957"
     CDS             1..1298
                     /gene="S"
                     /coded_by="HQ166910.1:20951..24847"
ORIGIN
        1 msfivaftvl lpivtaapsf aggcktysls gaytennyti ngtvsyglyy pdaifrsnvs
       61 vlftrpflpl haeayqwyga ykdqgvsiny qysylphpfk dgiavkifhr vregytkgfs
      121 tpaaylfgst fdsnsstlli gvngthriia vcqfvvcksp lvhlypynqt tppdtftkyy
      181 leglfsaadn csllieqplw ldnstnsnrl vtaqtqyift yesgvfsvyh ahnpngsvgy
      241 atlaftipvt ipitkfylpa vfdglkasgd ngvkrgnyhi efaylkrtty mftydgngyi
      301 tshvycaegp lqelkcsqls nnvppgvyrt tnyraepqgh vvryaadvad fqqscgaerl
      361 lnasidqipd pafwkrhvir nckfnfshim alshvydmqc ygidasklps tcwnevyadv
      421 frlaqddfys fkpsasgdla tynyklpsdf lgctliltnp nlycgnsttc gipgfngvtg
      481 dlhykvwrpg tticpmkyvn pgeqnamgyh cmsptehekk ltpvsfrggy yymyglaltl
      541 kpatvastvc dvtaqqtnlt ldkcvsytvy gyngqgilve tnetfpsfqn vqlwpngqlk
      601 afkdpqsnqv iavlpcaead vsvatagnht nevatlftga pcsgvqakll gvsttsmwrr
      661 isenttkgid tpvgclfgav lstsnstecq fslgldtcln itrgrvgsrs aghlkessty
      721 nyffqdmpke seipfsnftv eipdnftiai eyetlpirms kisvdcsryv cgtdvvcanq
      781 lvqygkfcdn inealrgvsl qqdsnvaell sdikqltrvs dldlkdingf nfssslyntdy
      841 ldatssgrrs aiedllfnkv vtadvgfmkk yeectggsvf kdldcaqsfn glkvlppqms
      901 dahvgvytta aamgsffsip ntmqmayrfn giavtqsvlv dnqkeiankf nqaltsiqqg
      961 ftatnsavqk lqdvvnanaa alntlvtqlg nnfgaissai nditqrldkl eaavqidrli
     1021 ngrlqvlqtf vtqqlimase irasaqlakq kmsecvlsqs krqdfcgrgl hlmsfpqsap
     1081 qgmvflhvly rptsyinvts tpaicsenka yfptdgvfvl hdnqwmitkr nfydpvnisl
     1141 snvryagscd vittyanhti fepdnstlqd fmheleeirk nlsmsapnsp nftlpglsdi
     1201 nasfvdlske metlqnvvrq lnksvidlke lgtyeyyekw pwyiwlgfia glvaialvlv
     1261 licstsccs cfkgmcsckk ccdsydddeq ilikqhyp
//
```